Genome-based phylogenetic analysis of Streptomyces and its relatives

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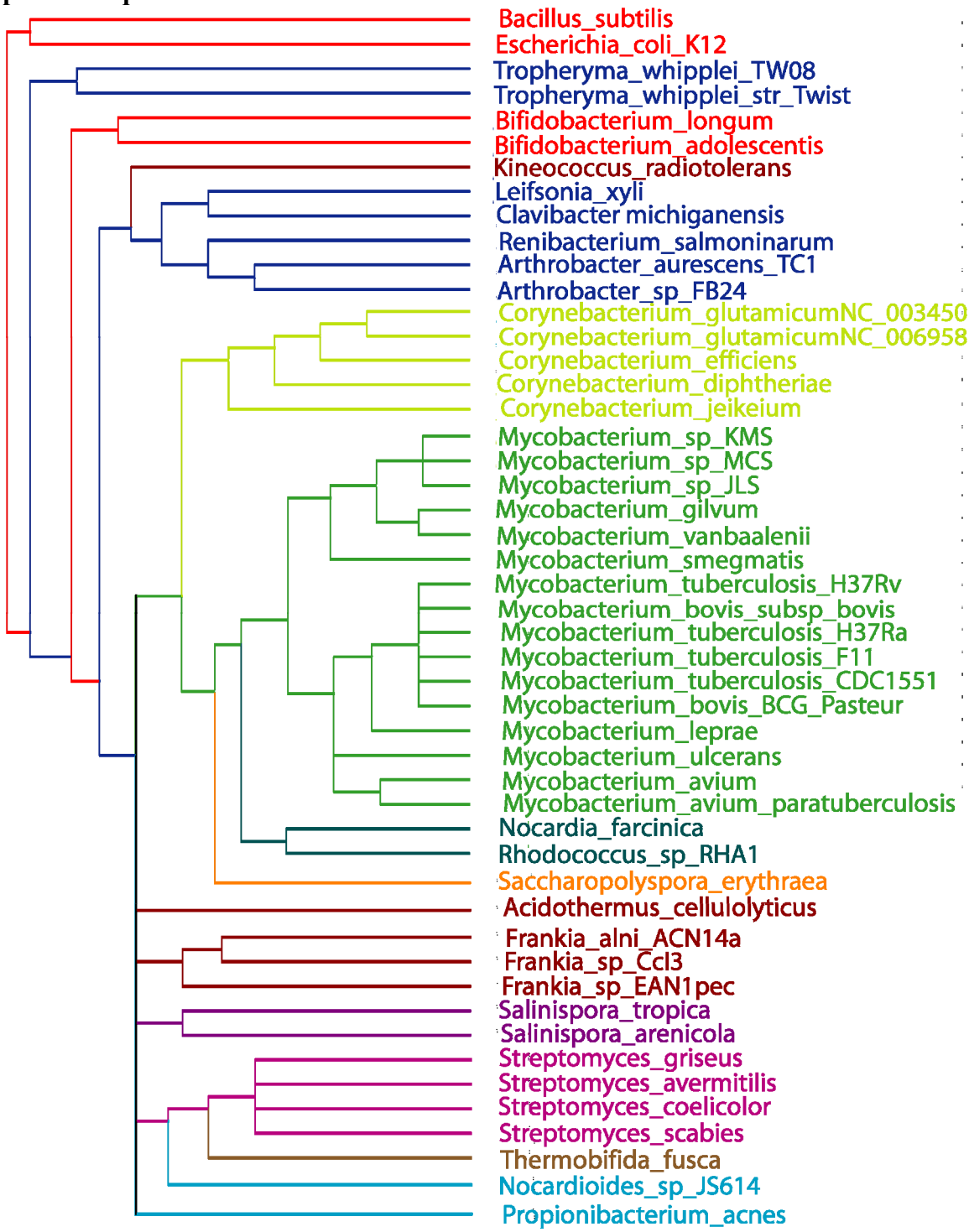
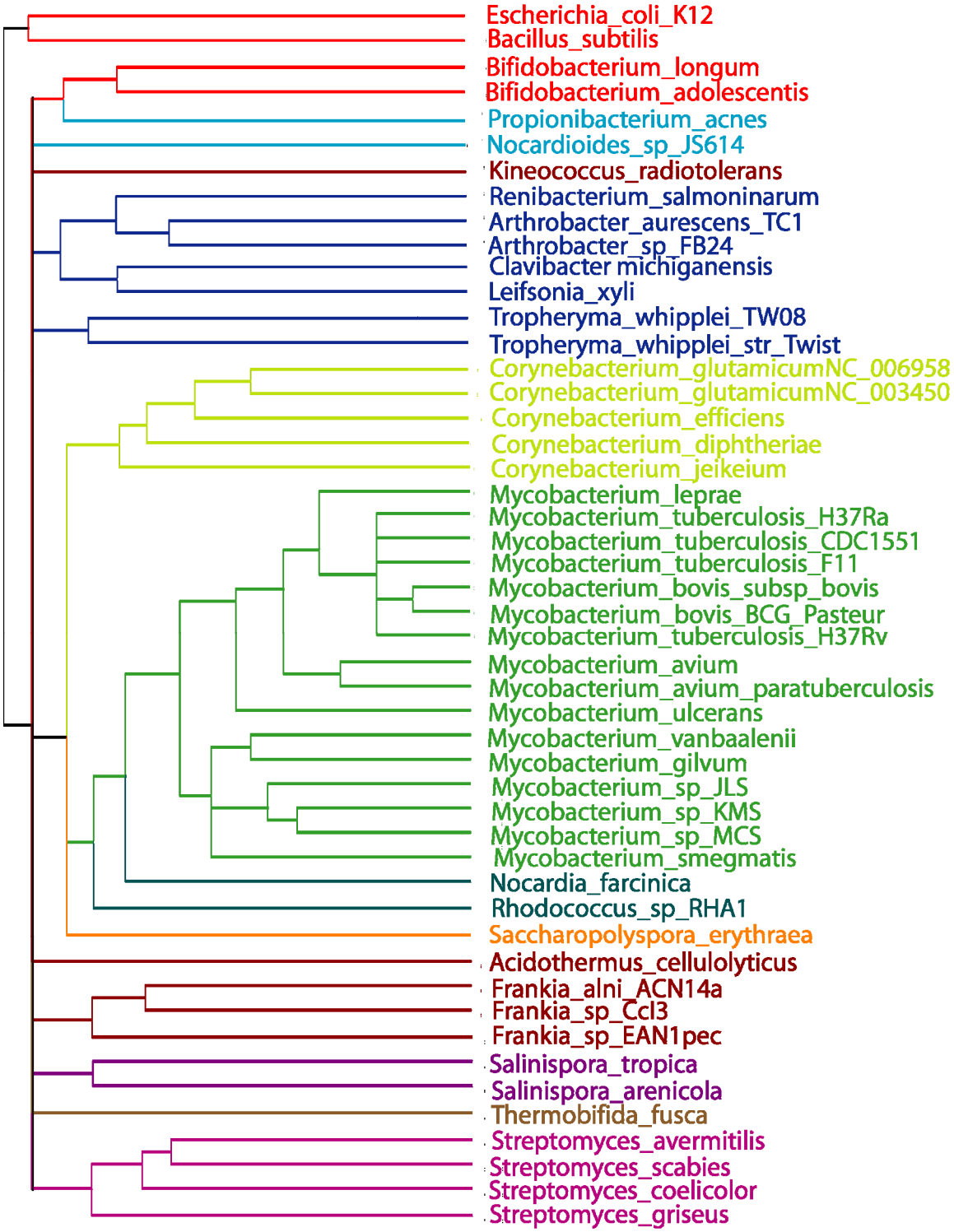
Supplementary Material Fig 1. Consensus tree based on DNA Topoisomerase protein sequence



Initial trees were reconstructed using four tree inference approaches (NJ, Fitch, ML, PARS) with 100 bootstrap replicates each and combined by majority-rule consensus to include only well-supported branches. Organisms having the same colors are members of the same suborder in the taxonomical classification of NCBI.

Supplementary Material Fig 2. Consensus tree based on GTPase protein sequence



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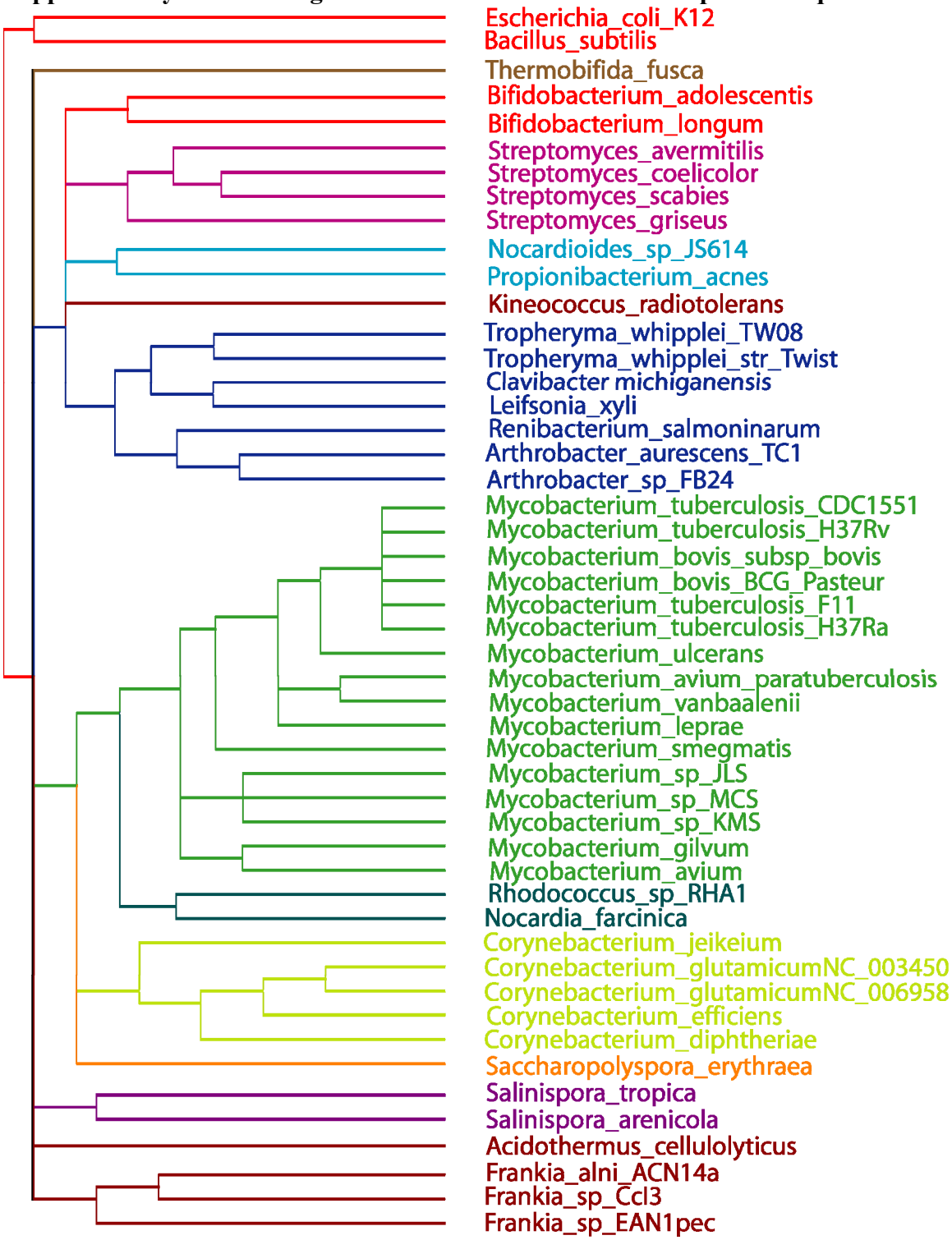
Supplementary Material Fig 3. Consensus tree based on SecY protein sequence



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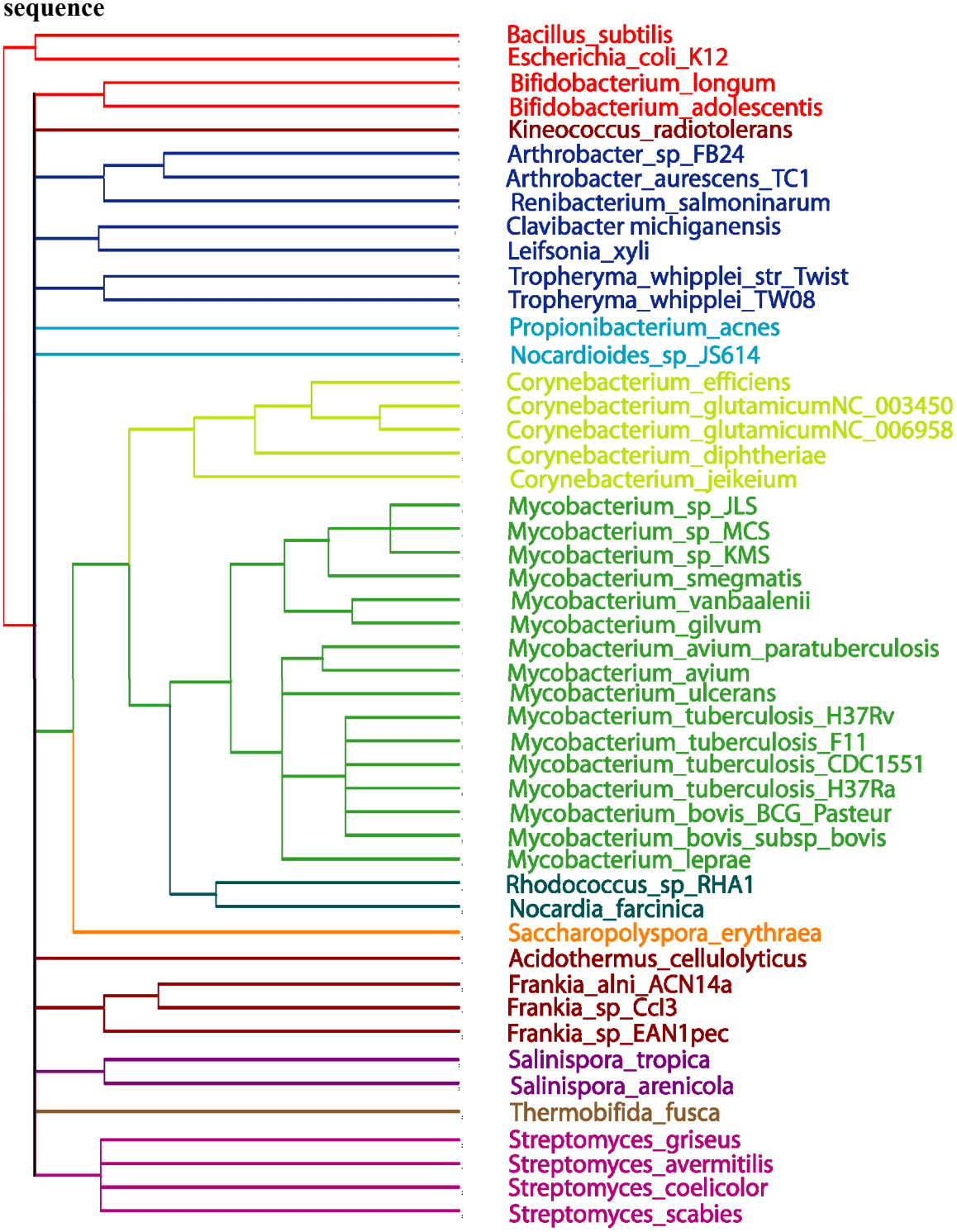
Supplementary Material Fig 4. Consensus tree based on Ribosomal RNA S1 sequence



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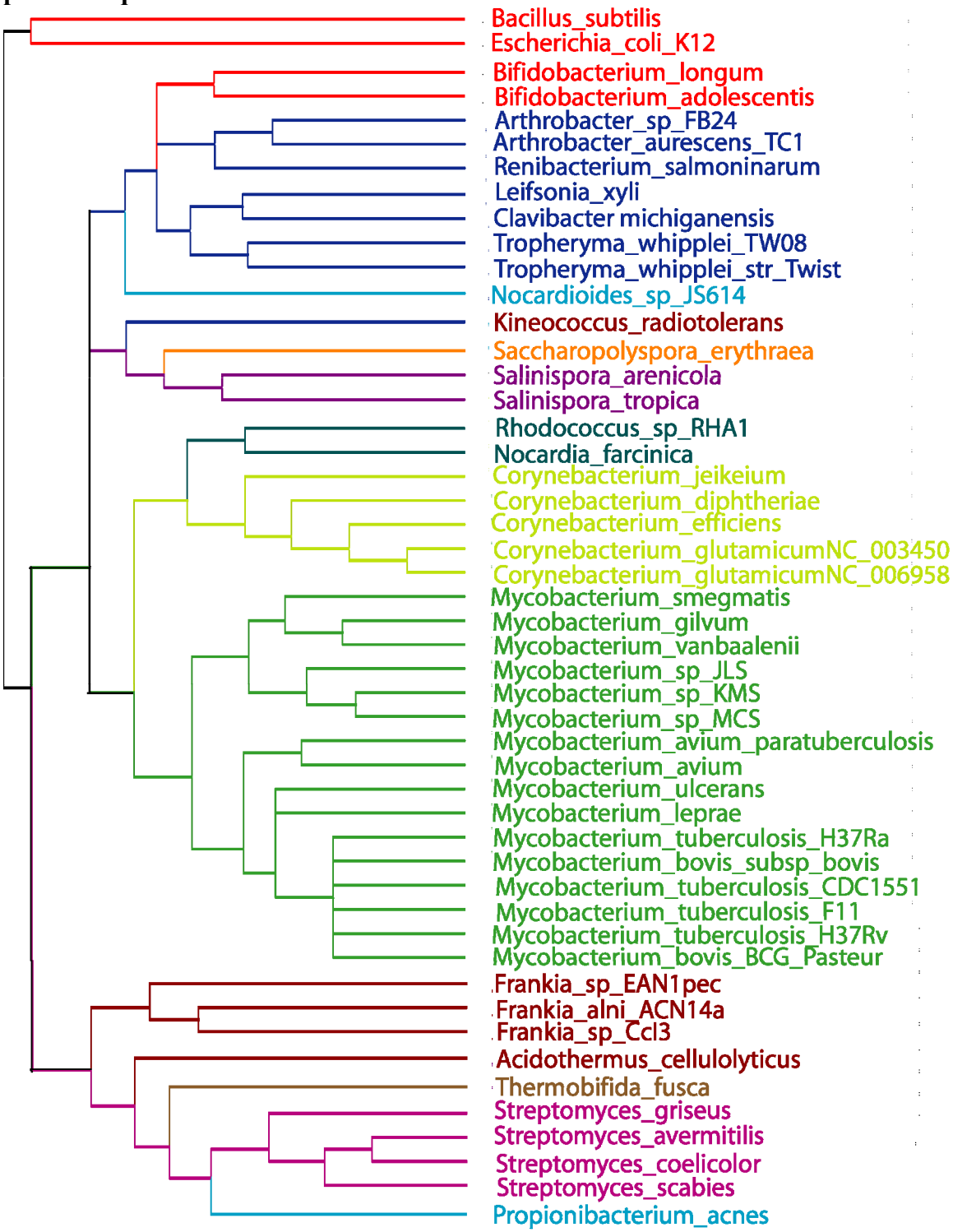
Supplementary Material Fig 5. Consensus tree based on Isoleucyl tRNA synthetase protein sequence



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